

FIG. 1

Sequence of human APRIL (SEQ ID NOS: 1 and 2)

Human G70 cDNA (SEQ ID NO 1)

Length: 1465 bp

1 GCCAACCTTC CCTCCCCCAA CCCTGGGGGCC GCCCCAGGGT TCCTGCGCAC
51 TGCCTGTTCC TCCTGGGTGT CACTGGCAGC CCTGTCCTTC CTAGAGGGAC
101 TGGAACCTAA TTCTCCTGAG GCTGAGGGAG GGTGGAGGGT CTCAAGGCAA
151 CGCTGGCCCC ACGACGGAGT GCCAGGAGCA CTAACAGTAC CCTTAGCTTG
201 CTTTCCTCCT CCCTCCTTTT TATTTTCAAG TTCCTTTTAA TTTCTCCTTG
251 CGTAACAACC TTCTTCCCTT CTGCACCACT GCCCGTACCC TTACCCGCCC
301 CGCCACCTCC TTGCTACCCC ACTCTTGAAA CCACAGCTGT TGGCAGGGTC
351 CCCAGCTCAT GCCAGCCTCA TCTCCTTTCT TGCTAGCCCC CAAAGGGCCT
401 CCAGGCAACA TGGGGGGGCC AGTCAGAGAG CCGGCACTCT CAGTTGCCCT
451 CTGGTTGAGT TGGGGGGCAG CTCTGGGGGC CGTGGCTTGT GCCATGGCTC
501 TGCTGACCCA ACAAACAGAG CTGCAGAGCC TCAGGAGAGA GGTGAGCCGG
551 CTGCAGGGGA CAGGAGGCC CTCCCAGAAT GGGGAAGGGT ATCCCTGGCA
601 GAGTCTCCCG GAGCAGAGTT CCGATGCCCT GGAAGCCTGG GAGAGTGGGG
651 AGAGATCCCG GAAAAGGAGA GCAGTGCTCA CCCAAAAACA GAAGAAGCAG
701 CACTCTGTCC TGCACCTGGT TCCCATTAAAC GCCACCTCCA AGGATGACTC
751 CGATGTGACA GAGGTGATGT GGCAACCAGC TCTTAGGCGT GGGAGAGGCC
801 TACAGGCCCA AGGATATGGT GTCCGAATCC AGGATGCTGG AGTTTATCTG
851 CTGTATAGCC AGGTCCTGTT TCAAGACGTG ACTTTCACCA TGGGTCAGGT
901 GGTGTCTCGA GAAGGCCAAG GAAGGCAGGA GACTCTATTC CGATGTATAA
951 GAAGTATGCC CTCCCACCCG GACCGGGCCT ACAACAGCTG CTATAGCGCA
1001 GGTGTCTTCC ATTTACACCA AGGGGATATT CTGAGTGTC TAATTCCCCG
1051 GGCAAGGGCG AAACCTAACC TCTCTCCACA TGGAACCTTC CTGGGGTTTG
1101 TGAAACTGTG ATTGTGTTAT AAAAAGTGGC TCCCAGCTTG GAAGACCAGG
1151 GTGGGTACAT ACTGGAGACA GCCAAGAGCT GAGTATATAA AGGAGAGGGA
1201 ATGTGCAGGA ACAGAGGCGT CTTCCTGGGT TTGGCTCCCC GTTCCTCACT
1251 TTTCCCTTTT CATTCACC CCCTAGACTT TGATTTTACG GATATCTTGC
1301 TTCTGTTCCC CATGGAGCTC CGAATTCTTG CGTGTGTGTA GATGAGGGGC
1351 GGGGGACGGG CGCCAGGCAT TGTTCAAGACC TGGTCGGGGC CCACTGGAAG
1401 CATCCAGAAC AGCACCACCA TCTAACGGCC GCTCGAGGGA AGCACCCGGC
1451 GGTTTGGGCG AAGTC

The proposed transmembrane domains are boxed

human G70 protein sequence (SEQ ID NO 2)

1 MPASSPFLLA PKGPPGNMGG PVREPALSVA LWLSWGAALG AVACAMALLT
51 QQTELQSLRR EVSRLQGTGG PSQNGEGYPW QSLPEQSSDA LEAWESGERS
101 RKRRAVLTQK QKKQHSVLHL VPINATSKDD SDVTEVMWQP ALRRGRGLQA
151 QGYGVRIQDA GYLLYSQVL FQDVTFTMGQ VVSREGQGRQ ETLFRCIRSM
201 PSHPDRAYNS CYSAGVFHLH QGDILSVIIP RARAKLNLSP HGTFLLGFV

FIG. 2A

Sequence of mouse G70 (SEQ ID NOS: 3 and 4)

Mouse G70 (SEQ ID NO 3)

```
1  CATGCCGAGT GCTTTGTGTG TGTTACCTGC TCTAAGAAGC TGGCTGGGCA
51  GCGTTTCACC GCTGTGGAGG ACCAGTATTA CTGCGTGGAT TGCTACAAGA
101 ACTTTGTGGC CAAGAAGTGT GCTGGATGCA AGAACCCCAT CACTGGGTTT
151 GGTAAAGGCT CCAGTGTGGT GGCCTATGAA GGACAATCCT GGCACGACTA
201 CTGCTTCCAC TGCAAAAAAT GCTCCGTGAA TCTGGCCAAC AAGCGCTTTG
251 TATTTCATAA TGAGCAGGTG TATTGCCCTG ACTGTGCCAA AAAGCTGTAA
301 CTTGACGGCT GCCCTGTCTT TCCTAGATAA TGGCACCAAA TTCTCCTGAG
351 GCTAGGGGGG AAGGAGTGTC AGAGTGTAC TAGCTCGACC CTGGGGACAA
401 GGGGGACTAA TAGTACCCTA GCTTGATTTC TTCCTATTCT CAAGTTCCTT
451 TTTATTTCTC CCTTGCGTAA CCCGCTCTTC CCTTCTGTGC CTTTGCCTGT
501 ATTCCCACCC TCCCTGCTAC CTCTTGGCCA CCTCACTTCT GAGACCACAG
551 CTGTTGGCAG GGTCCCTAGC TCATGCCAGC CTCATCTCCA GGCCACATGG
601 GGGGCTCAGT CAGAGAGCCA GCCCTTTCGG TTGCTCTTTG GTTGAGTTGG
651 GGGGCAGTTC TGGGGGCTGT GACTTGTGCT GTCGCACTAC TGATCCAACA
701 GACAGAGCTG CAAAGCCTAA GGCGGGAGGT GAGCCGGCTG CAGCGGAGTG
751 GAGGGCCTTC CCAGAAGCAG GGAGAGCGCC CATGGCAGAG CCTCTGGGAG
801 CAGAGTCCTG ATGTCCTGGA AGCCTGGAAG GATGGGGCGA AATCTCGGAG
851 AAGGAGAGCA GTACTCACCC AGAAGCACAA GAAGAAGCAC TCAGTCCTGC
901 ATCTTGTTCC AGTTAACATT ACCTCCAAGG ACTCTGACGT GACAGAGGTG
951 ATGTGGCAAC CAGTACTTAG GCGTGGGAGA GGCCTGGAGG CCCAGGGAGA
1001 CATTGTACGA GTCTGGGACA CTGGAATTTA TCTGCTCTAT AGTCAGGTCC
1051 TGTTTCATGA TGTGACTTTC ACAATGGGTC AGGTGGTATC TCGGGAAGGA
1101 CAAGGGAGAA GAGAACTCT ATTCCGATGT ATCAGAAGTA TGCCTTCTGA
1151 TCCTGACCGT GCCTACAATA GCTGCTACAG TGCAGGTGTC TTTCATTTAC
1201 ATCAAGGGGA TATTATCACT GTCAAAATTC CACGGGCAA CGCAAACTT
1251 AGCCTTTCTC CGCATGGAAC ATTCCTGGGG TTTGTGAAAC TATGATTGTT
1301 ATAAAGGGGG TGGGGATTTC CCATTCCAAA AACTGGCTAG ACAAAGGACA
1351 AGGAACGGTC AAGAACAGCT CTCCATGGCT TTGCCTTGAC TGTGTTCCT
1401 CCCTTTGCCT TTCCCGCTCC CACTATCTGG GCTTTGACTC CATGGATATT
1451 AAAAAAGTAG AATATTTTGT GTTTATCTCC CAAAAA
```

FIG. 2A

FIG. 2B

Mouse G70 Length: 241 (SEQ ID NO 4)

1 MPASSPGHMG GSVREPALSV ALWLSWGAVL GAVTCAVALL IQQTELOSLR
51 REVSRLQRRSG GPSQKQGERP WQSLWEQSPD VLEAWKDGAK SRRRRRAVLTO
101 KHKKKHLSVLH LVPVNITSKD SDVTEVMWQP VLRRGRGLEA QGDIVRVWDT
151 GIYLLYSQVL FHDVTFTMGQ VVSREGQGRR ETLFRCIRSM PSDPDRAVNS
201 CYSAGVFHLH QGDIITVKIP RANAKLSLSP HGTFLGFVKL *

G-70 FLAG des92 (smuG70) Strain #4081 (SEQ ID NO 19):

MDYKDDDDKKHKKKHSVLHLVPVNITSKDSDVTEVMWQPVLLRRGRGLEAQGDIVRVWDTGIY
LLYSQVLFHDVTFTMGQVVSREGQGRRETLFRCIRSMPSDPDRAYNSCYSAGVFHLHQGDII
TVKIPRANAKLSLSPHGTFLGFVKL*

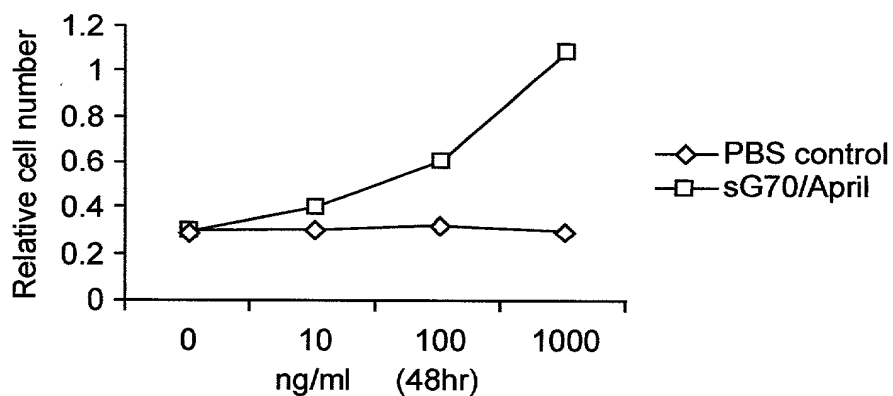
FIG. 3

Alignm. of human and mouse G70

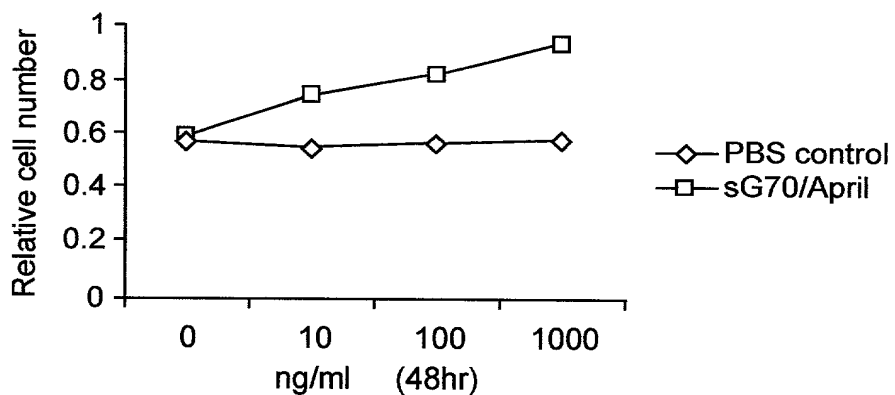
mouse:	1	MPASS-----PGHMGGS	VREPALSVALWLSWGAVLGAVTCAVALL	IQQTEQLQSLRR	51	
		MPASS	PG+MGG	VREPALSVALWLSWGA LGAV CA+ALL	QQTEQLQSLRR	
human:	1	MPASSPFLAPKGP	PPGNMG	GFVREPALSVALWLSWGAALGAVACAMALL	TQQTEQLQSLRR	
					60	
mouse:	52	EVSRLQ	RS	GGPSQKQGERPWQSLWEQSPDVLEAWKDGAKSRRRRRAVLTQKHKKKHSHVLHL	111	
		EVSRLQ	+GGPSQ	PWQSL EQS D LEAW+ G +SR+RRAVLTQK KK+HSHVLHL		
human:	61	EVSRLQ	GTGGPSQNGEGYPWQSLPEQSSDALEAWESGERSRKRRAVLTQKQKQKQHSHVLHL		120	
					111	
mouse:	112	VPVNIT	SKD-SDVTEVMWQP	VLRRGRGLEAQGDIVRVWDTGIYLLYSQVLFHDVTFTMGQ	170	
		VP+N	TSKD	SDVTEVMWQP LRRGRGL+AQG VR+ D G+YLLYSQVLF	DVTFTMGQ	
human:	121	VPINAT	SKDDSDVTEVMWQP	ALRRGRGLQAQGYGVRIQDAGVYLLYSQVLFQDVTFTMGQ	180	
					180	
mouse:	171	VVSREGQ	RRRETL	FR	CIRSMPSDPDRAYNSCYSAGVFHLHQGDIITVKIPRANAKLSLSP	230
		VVSREGQ	GR+ETL	FR	CIRSMPS PDRAYNSCYSAGVFHLHQGDI+V IPRA AKL+LSLSP	
human:	181	VVSREGQ	GRQETL	FR	CIRSMPSHPDRAYNSCYSAGVFHLHQGDILSVIIPRARA	KLNLSP
						240
mouse:	231	HG	FLG	FVKL	240	
		HG	FLG	FVKL		
human:	241	HG	FLG	FVKL	250	

FIG. 4A

Effect of sG70/April on Raji cell proliferation



Effect of sG70/April on Jurkat cell proliferation



Effect of sG70/April on K562 cell proliferation

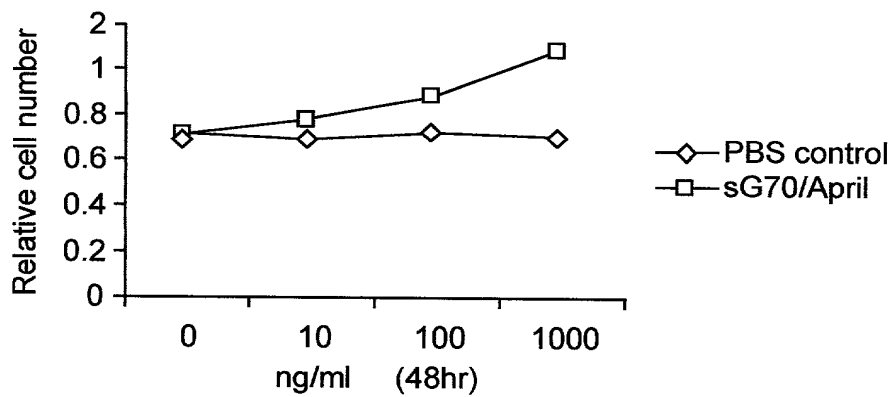
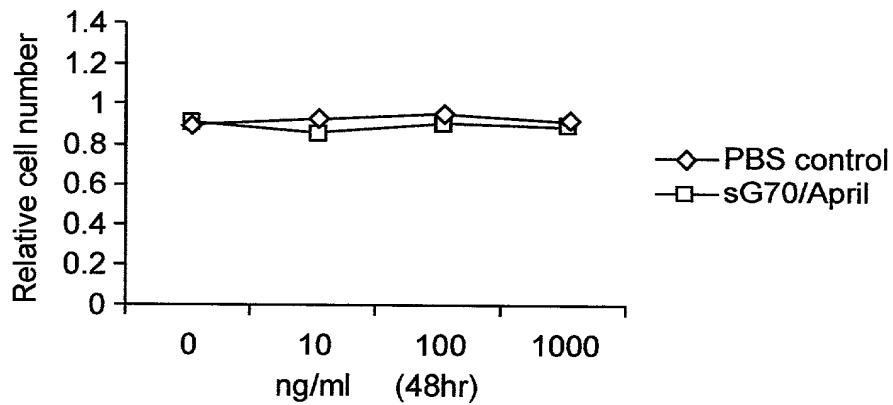
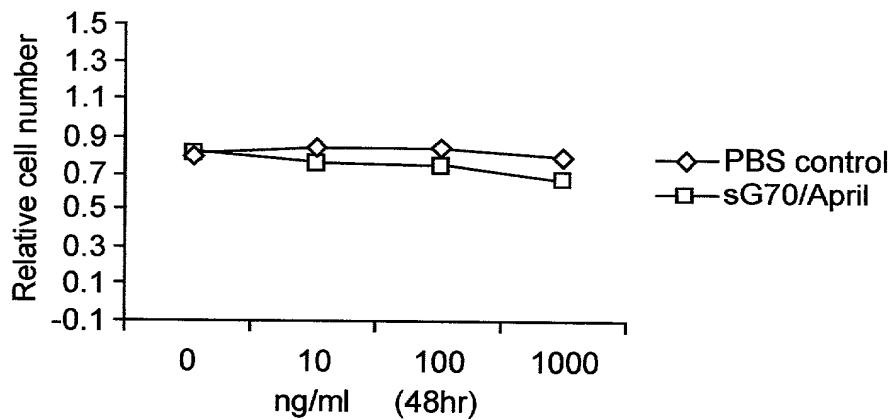


FIG. 4B

Effect of sG70/April on U937 cell proliferation



Effect of sG70/April on 293 T cell proliferation



Effect of sG70/April on 3T3 cell proliferation

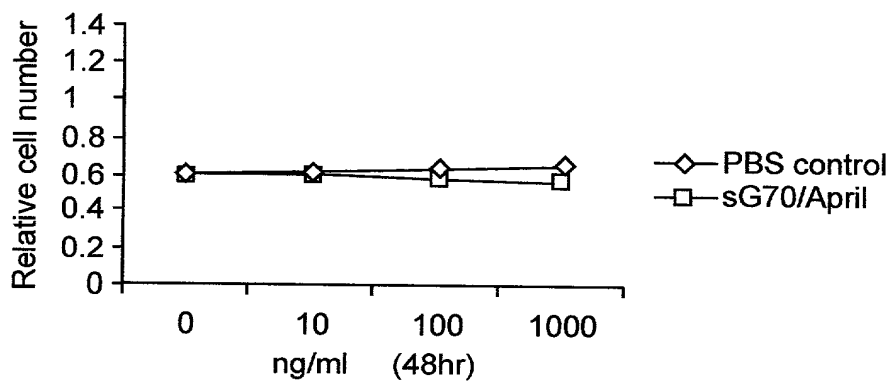


FIG. 5A

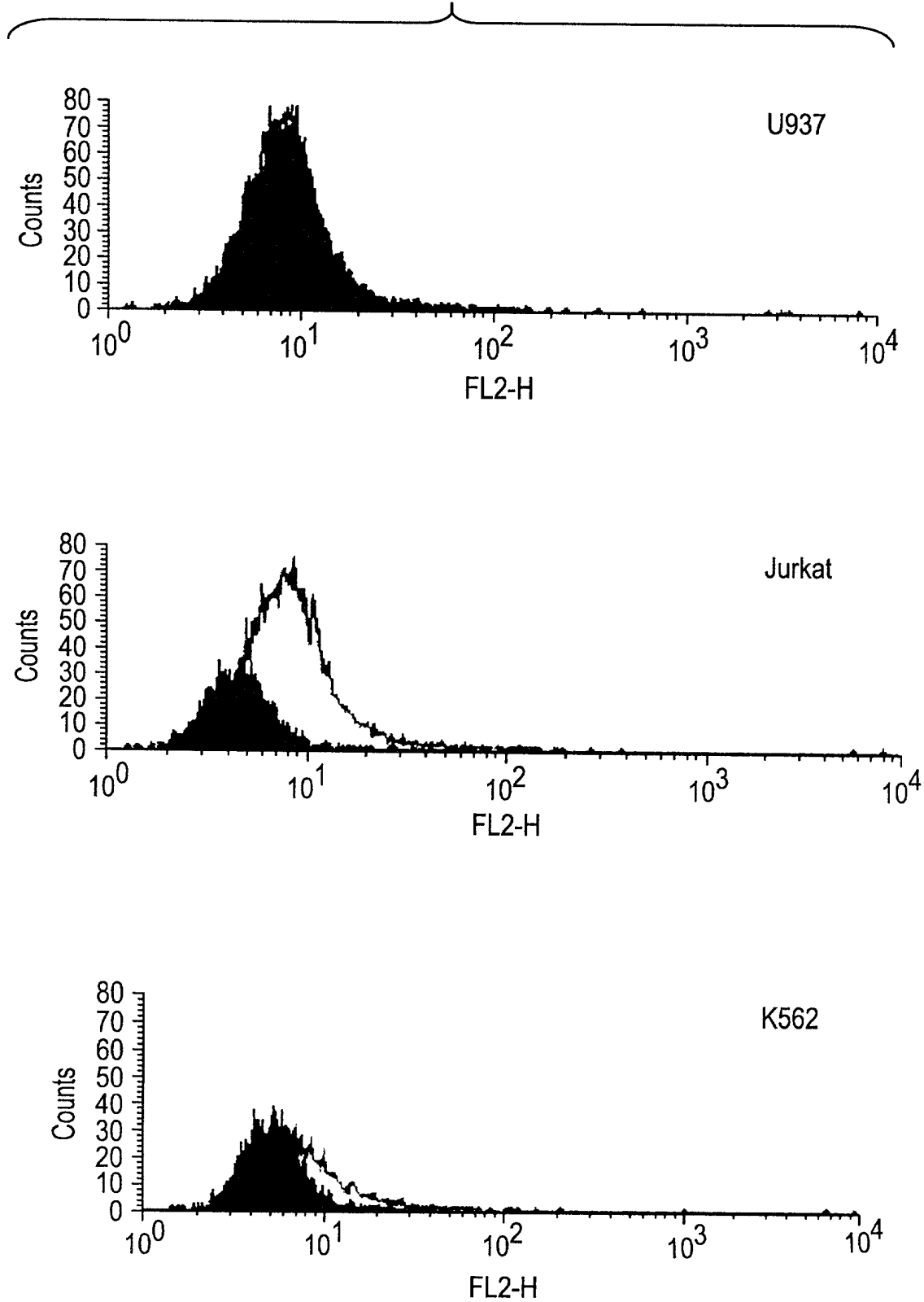


FIG. 5B-1

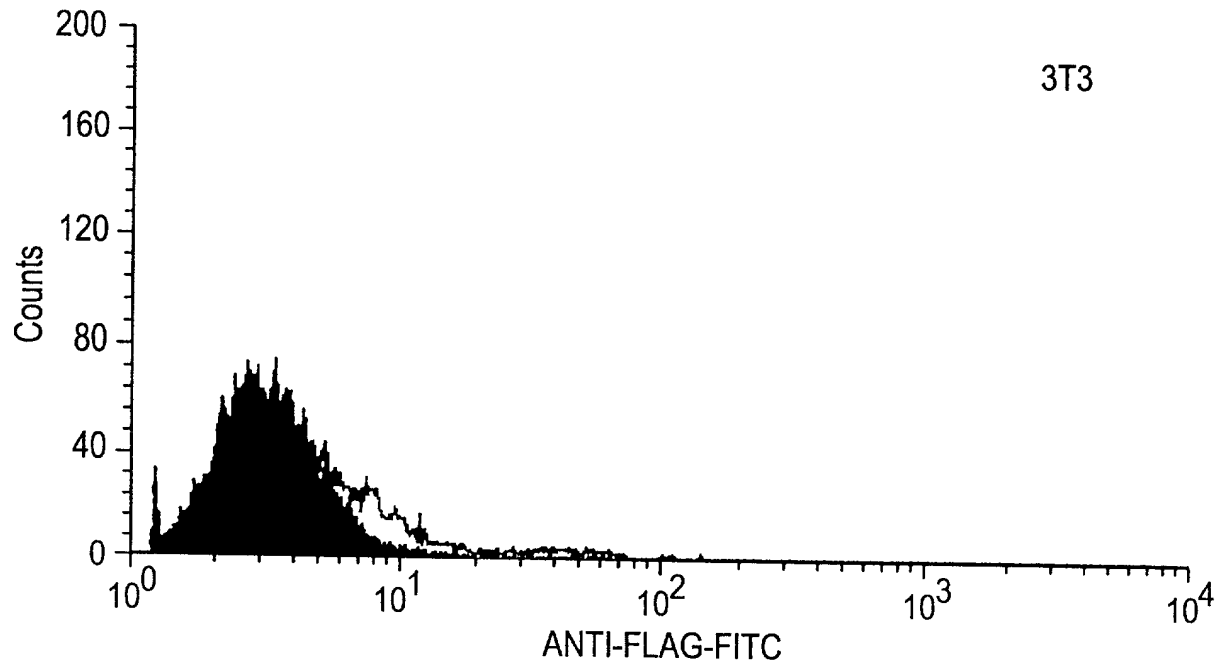


FIG. 5B-2

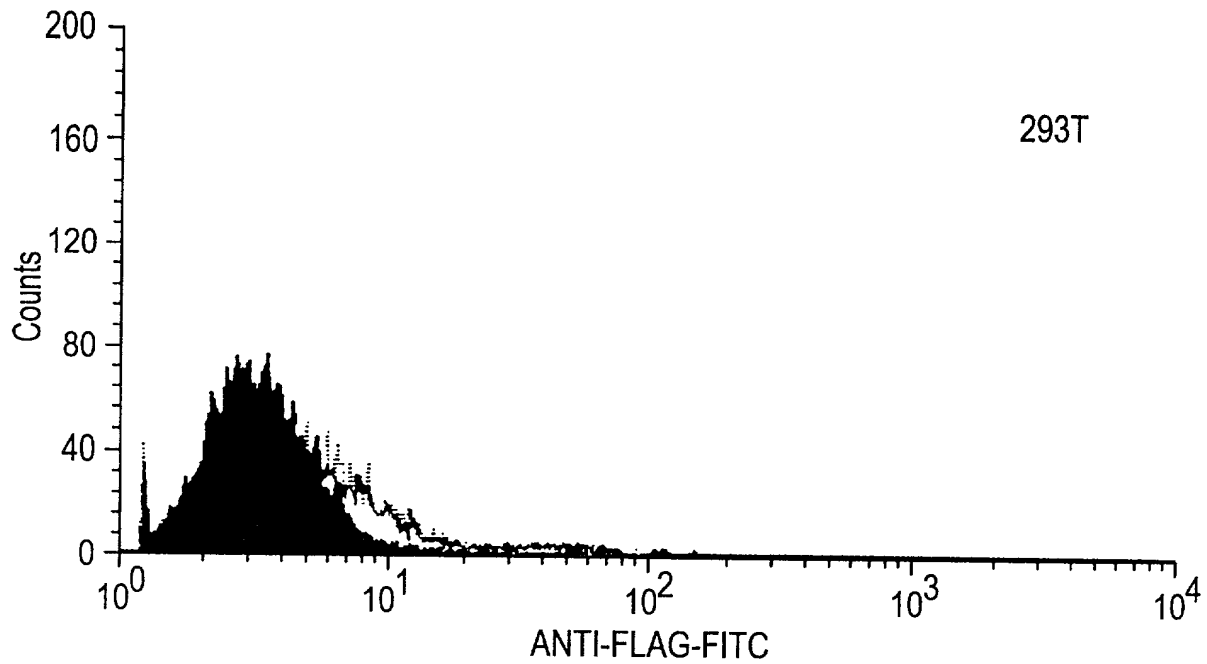


FIG. 5B-3

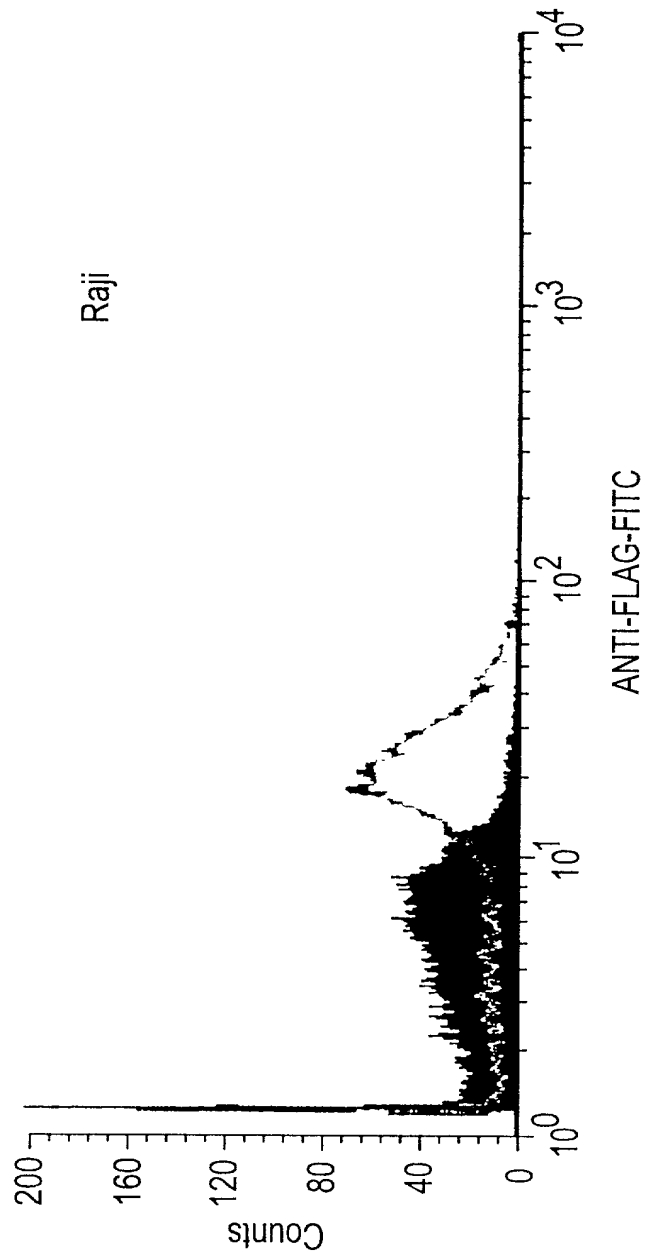
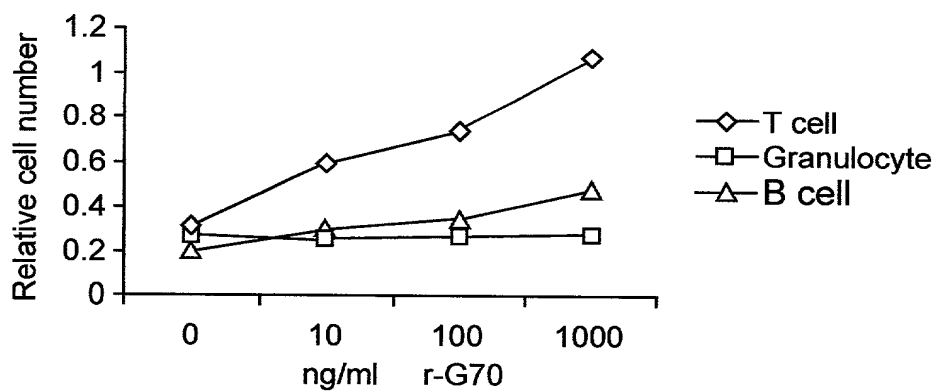


FIG. 6

The effect of r-G70/April on human
peripheral blood B cell, T cell and Granucolyte



The effect of IL-2 and G70/April on human
peripheral T cell proliferation

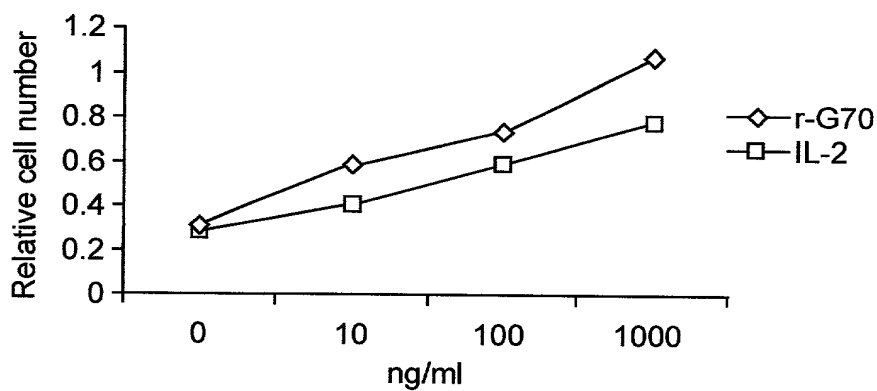
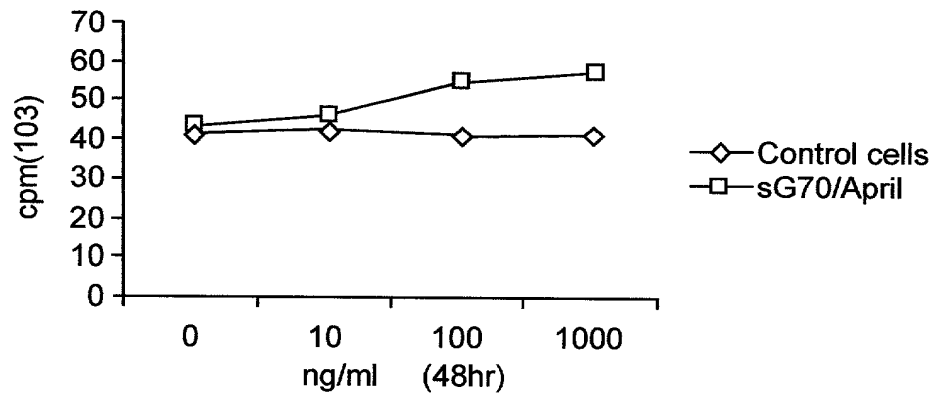


FIG. 7

Effect of sG70/April on murine B cell proliferation



Effect of sG70/April on murine T cell proliferation

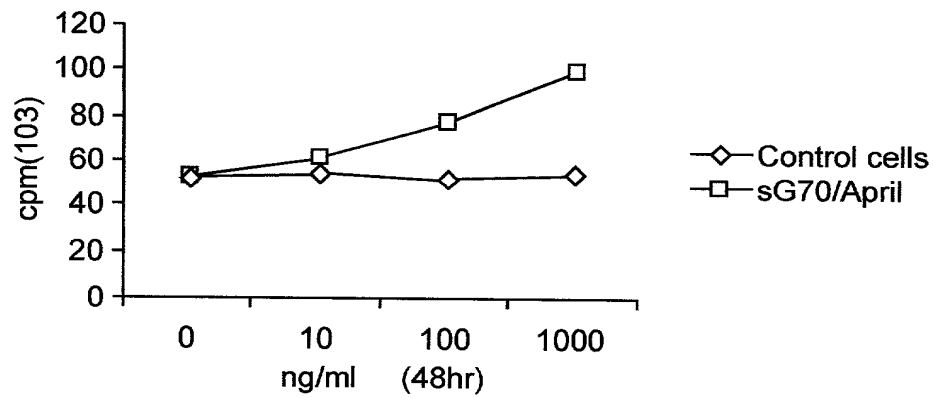


FIG. 8

Effect of G70/April on murine T cell
proliferation costimulated through CD28
antibody

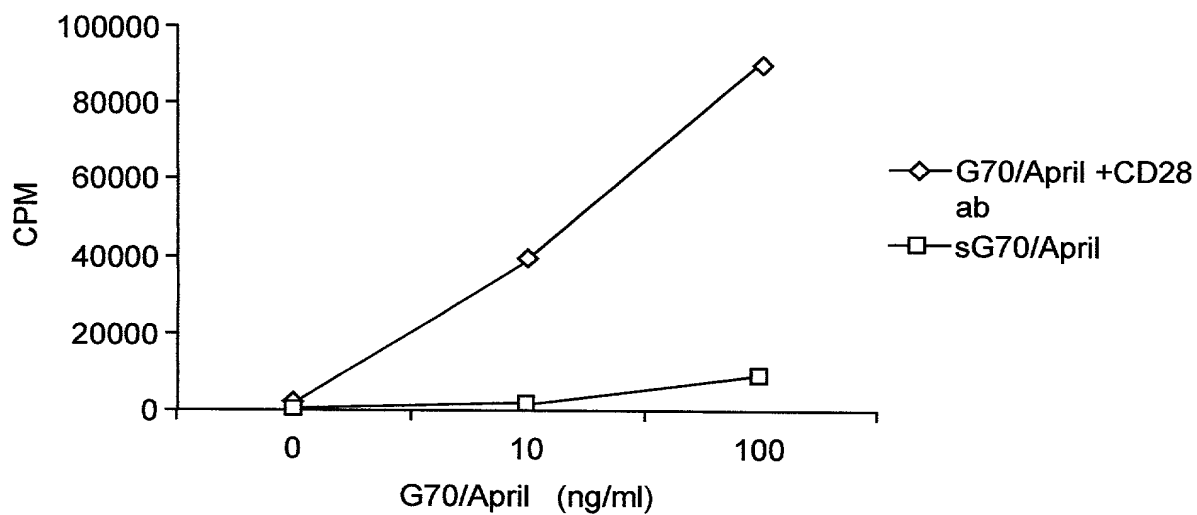
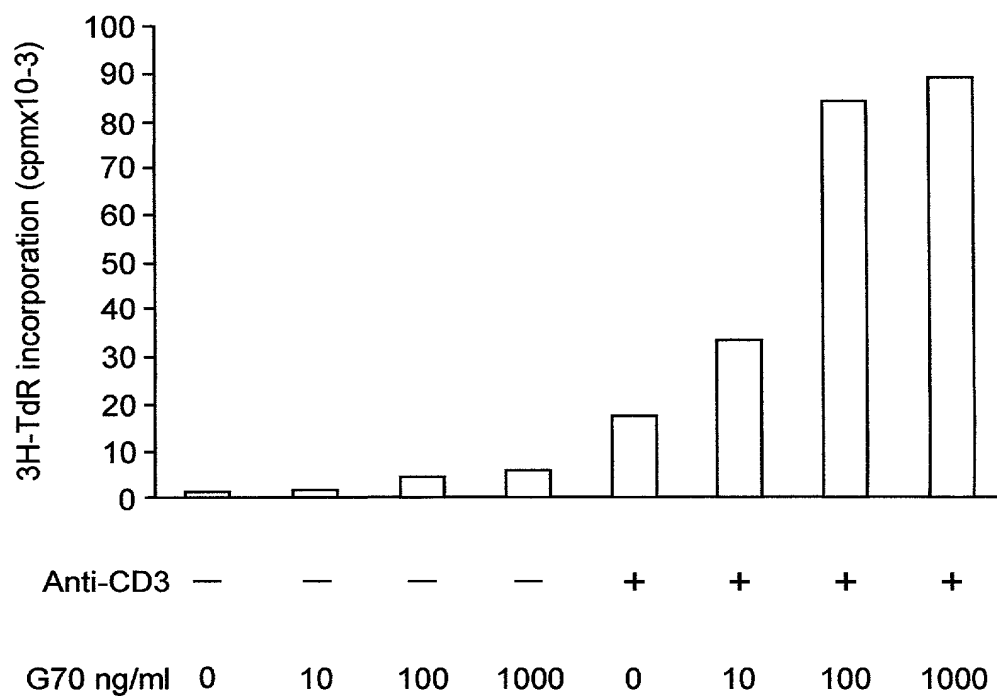


FIG. 9

Co-stimulatory activity of G70/April on mouse T cells



Human BCMA

Human (SEQ ID NO: 5):

1 MAGQCSQNEY FDSL LHACIP CQLRCSSNTP PLTCQRYCNA SVTNSVKGTN
51 AILWTCGLGS LIISLAVFVL MFLLRKISSE PLKDEFKNTG SGLLGMANID
101 LEKSRTGDEI ILPRGLEYTV EECTCEDCIK SKPKVDSHC FPLPAMEEGA
151 TILVTTKTND YCKSLPAALS ATEIEKSISA R

Human (SEQ ID NO: 5):

MAGQ**CSQ** **NEYFDSLLHA** **CIPCQLRCSS** **NTPPLTCQRY** CNASVTNSVK
GTNA ILWTCL GLSLIISLAV FVLMFLLRKI SSEPLKDEFK NTGSGLLGMA
NIDLEKSRTG DEIILPRGLE YTVEECTCED CIKSKPKVDS DHCFLPLAME
EGATILVTTK TNDYCKSLPA ALSATEIEKS ISAR

hBCMA's extracellular domain (SEQ ID NO: 6):

MAGQCSQ NEYFDSLHA CIPCQLRCSS NTPPLTCQRY CNASVTNSVK
GTNA

hBCMA's cysteine-rich consensus region (SEQ ID NO: 7):

CSQ NEYFDSLHA CIPCQLRCSS NTPPLTCQRY C

hBCMA's transmembrane region (SEQ ID NO: 8):

ILWTCL GLSLIISLAV FVLME

FIG. 10B

huBCMA-Fc (SEQ ID NO: 9):

MAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAGGG
GGDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK
FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKAL
PAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNG
QPENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFSQSVMEALHNHYTQKS
LSLSPGK*

muBCMA-Fc (SEQ ID NO: 10):

MAQQCFHSEYFDSLLHACKPCHLRCSNPPATCQPYCDPSVTSSVKGSYTGGGGG
DKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN
WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA
PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP
ENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFSQSVMEALHNHYTQKSLS
LSPGK*

FIG. 11

Alignment of human BCMA amino acid sequence and murine BCMA amino acid sequence

murine BCMA amino acid sequence Length: 185 (SEQ ID NO: 11):

1 MAQQCFHSEY FDSLHACKP CHLRCSNPPA TCQPYCDPSV TSSVKGYTYV
51 LWIFLGLTLV LSLALFTISF LLRKMNPEAL KDEPQSPGQL DGSQAQDKAD
101 TELTRIRAGD DRIFPRSLEY TVEECTCEDC VKSKPKGSD HFFPLPAMEE
151 GATILVTTKT GDYKSSVPT ALQSVGMGEK PTHTR

alignment of human BCMA amino acid sequence and murine BCMA amino acid sequence.

Query: 4 MAGQCSQNEYFD~~SL~~LHACIPCQ~~L~~RCSSTPPLTCQRYCNASVTNSVKG~~T~~NAI~~L~~WTC~~L~~GLS 63

MA Q~~C~~ +EYFD~~SL~~LHAC PC LRCS+ PP TCQ YC+ SVT+SVKGT +LW LGL+

Sbjct: 1 MAQQCFHSEYFD~~SL~~LHACKPKCHLRCSN--PPATCQPYCDDPSVTSSVKGTYTVLWIFLGLT 58

Query: 64 LIISLAVFVLMFLLRKISSEPLKDEFKNTG----SGLLGMANIDLEKSR~~T~~GDEI~~L~~PRGL 119

L++SLA+F + FLLRK++ E LKDE ++ G S L A+ +L + R GD+ I PR L

Sbjct: 59 LVLSLALFTISFLLRKMNPEALKDEPQSPGQLDGSQAQDKADTELTRIRAGDDRI~~F~~PRSL 118

Query: 120 EYTVEECTCEDCIKSKPKVDS~~D~~HCFFLPAMEEGATILVT~~T~~KNDYCKS-LPAAL-SATEI 177

EYTVEECTCEDC+KSKPK DSDH FPLPAMEEGATILVT~~T~~KT DY KS +P AL S +

Sbjct: 119 EYTVEECTCEDCVKSKPKGSD~~D~~HFFPLPAMEEGATILVT~~T~~KTGDYKSSVPTALQSV~~M~~GM 178

Query: 178 EKSISAR 184

EK R

Sbjct: 179 EKPTHTR 185

FIG. 12A

Human TACI

huTACI (SEQ ID NO: 14).

1 MSGLGRSRRG GRSRVDQEER FPQGLWTGVA MRSCPEEQYW DPLLGTCMSC
51 KTICNHQSQR TCAAFCRSLS CRKEQGKFYD HLLRDCISCA SICGQHPKQC
101 AYFCENKLRS PVNLPPELRR QRSGEVENNS DNSGRYQGLE HRGSEASPAL
151 PGLKLSADQV ALVYSTLGLC LCAVLCCFLV AVACFLKKRG DPCSCQPRSR
201 PRQSPAKSSQ DHAMEAGSPV STSPEPVETC SFCFPECRAP TQESAVTPGT
251 PDPTCAGRWG CHTRTTVLQP CPHIPDSGLG IVCVPAQEGG PGA

MSGLGRSRRGGRSRVDQEERFPQGLWTGVAMRSCPEEQYWDPLLGTCMSC
KTICNHQSQRTCAAFCRSLS**CRKEQGKFYD**HLLRDCISCAS**ICGQHPKQC**
AYFCENKLRSPVNLPPELRRQRSGEVENNSDNSGRYQGLE**HRGSEASPAL**
PGLKLSADQVALVYSTLGLCLCAVLCCFLVAVACFLKKRGDPCSCQPRSR
PRQSPAKSSQDHAMEAGSPVSTSPEPVETCSFCFPECRAP**TQESAVTPGT**
PDPTCAGRWGCHTRTTVLQPCPHIPDSGLGIVCVPAQEGGPGA

huTACI's extracellular domain (SEQ ID NO: 15):

1 MSGLGRSRRG GRSRVDQEER FPQGLWTGVA MRSCPEEQYW DPLLGTCMSC
51 KTICNHQSQR TCAAFCRSLS CRKEQGKFYD HLLRDCISCA SICGQHPKQC
101 AYFCENKLRS PVNLPPELRR QRSGEVENNS DNSGRYQGLE HRGSEASPAL
151 PGLKLSADQV ALVYST

FIG. 12B

huTACI's cysteine-rich consensus region (SEQ ID NO: 16):

CPEEQYWDPLLGTCSCKTICNHQSQR TCAAF C and
CRKEQGKFYDHLLRDCISCASICGQHPKQCA YFC

transmembrane region (SEQ ID NO: 17):

LGLCLCAVLCCFLVAVACFL

hTACI-Fc (SEQ ID NO: 18):

1 MSGLGRSRRG GRSRVDQEER FPQGLWTGVA MRSCPEEQYW DPLLGTCSMC
51 KTICNHQSQR TCAAFCRSL S CRKEQGKFYD HLLRDCISCA SICGQHPKQC
101 AYFCENKLRS PVNLPPELRR QRSGEVENNS DNSGRYQGLE HRGSEASPAL
151 PGLKLSADQV ALVYSGGGGG DKTHTCPPCP APELLGGPSV FLFPPKPKDT
201 LMISRTPEVT CVVVDVSHED PEVKFNWYVD GVEVHNAKTK PREEQYNSTY
251 RVVSVLTVLH QDWLNGKEYK CKVSNKALPA PIEKTISKAK GQPREPQVYT
301 LPPSRDELTK NQVSLTCLVK GFYPSDIAVE WESNGQPENN YKTTTPVLDS
351 DGSFFLYSKL TVDKSRWQQG NVFSCSV MHE ALHNHYTQKS LSLSPGK*

FIG. 13

Alignment of cysteine rich extracellular regions of human TACI and human BCMA.

```
34 CPEEQYWDPLLGTCSCKTICNHQS.QRTCAAFCSRSLSCRKEQGKFYDHL 82
   | : :|. | || |. |. |. . || :| . . | . :
8  CSQNEYFDSLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGT..NAI 55
      .
      83 LRDCISCASI 92
      | | : . |
      56 LWTCLGLSLI 65
```

FIG. 14A

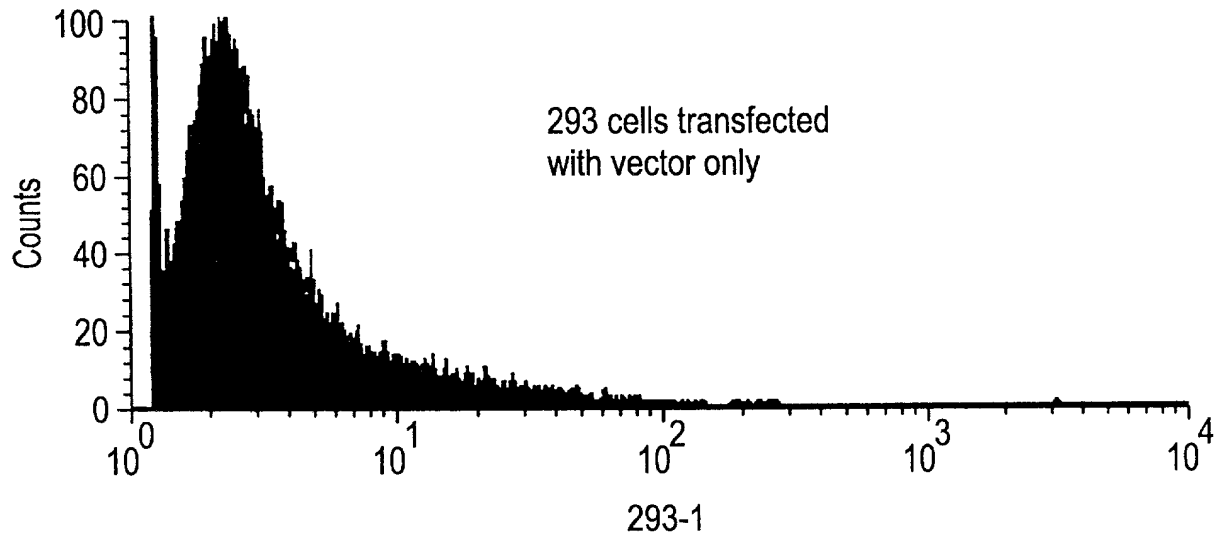


FIG. 14B

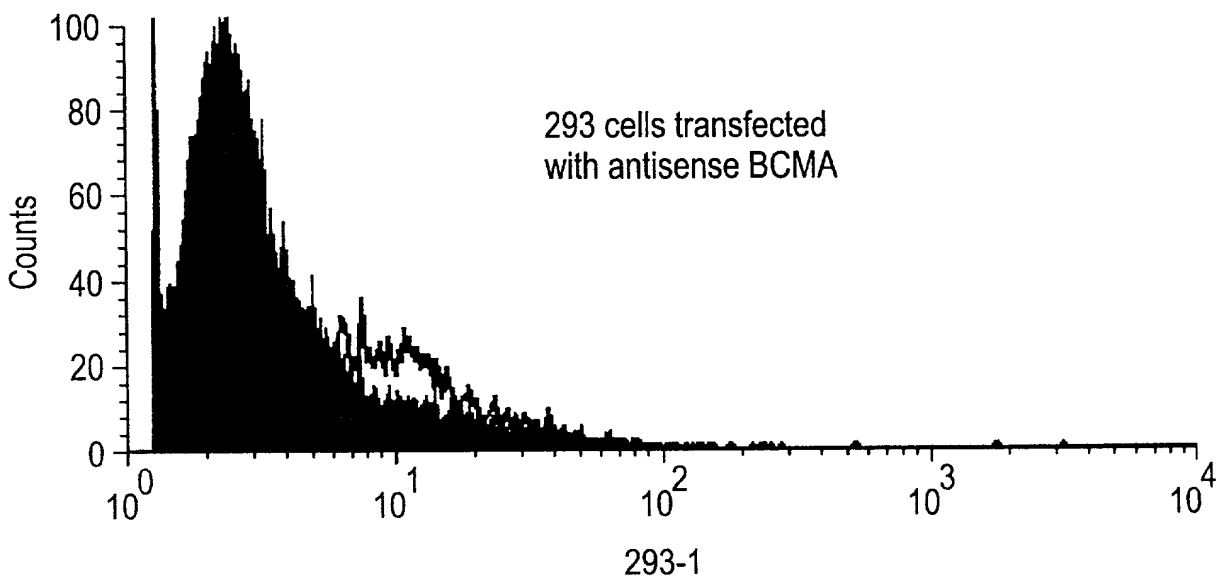


FIG. 14C

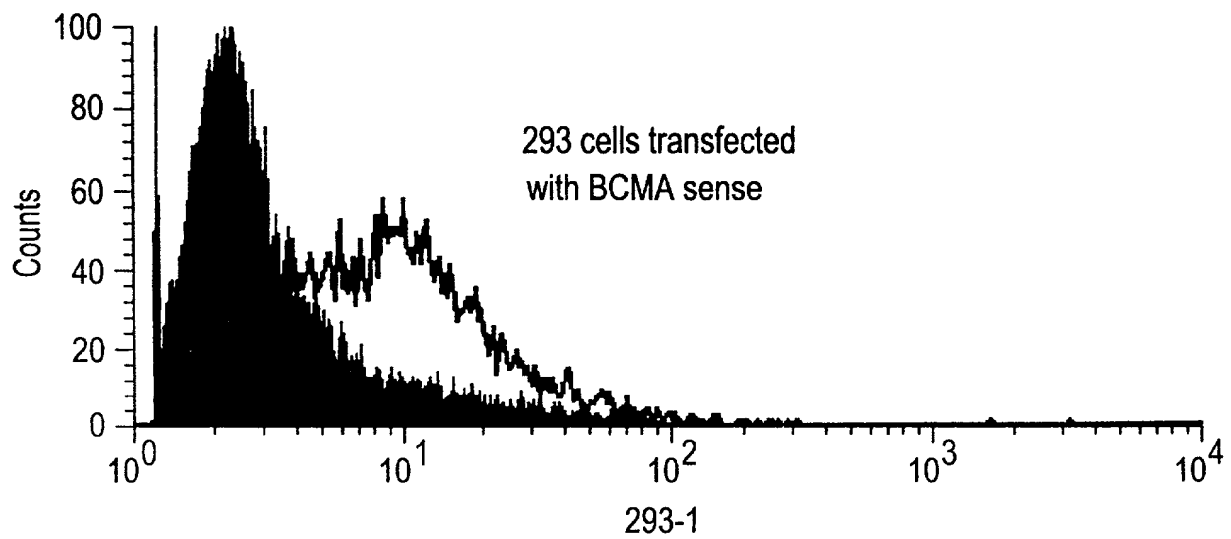


FIG. 15A

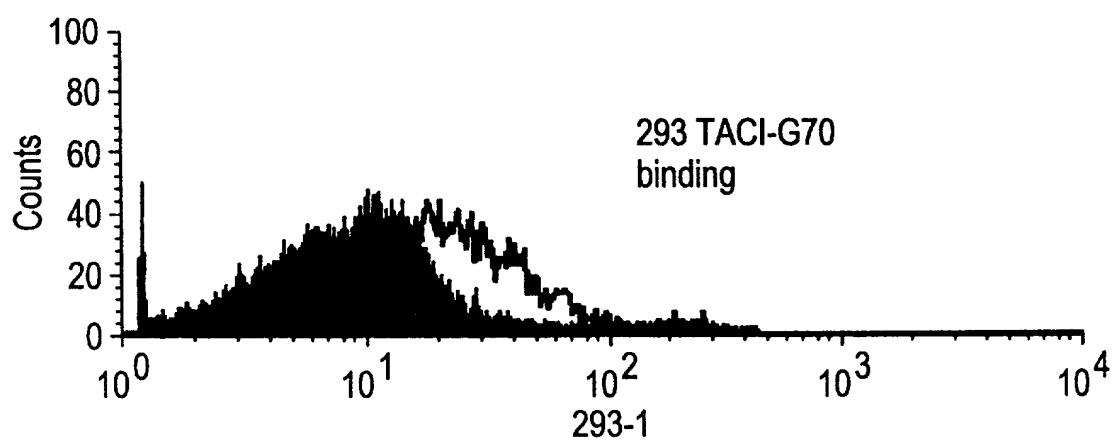


FIG. 15B

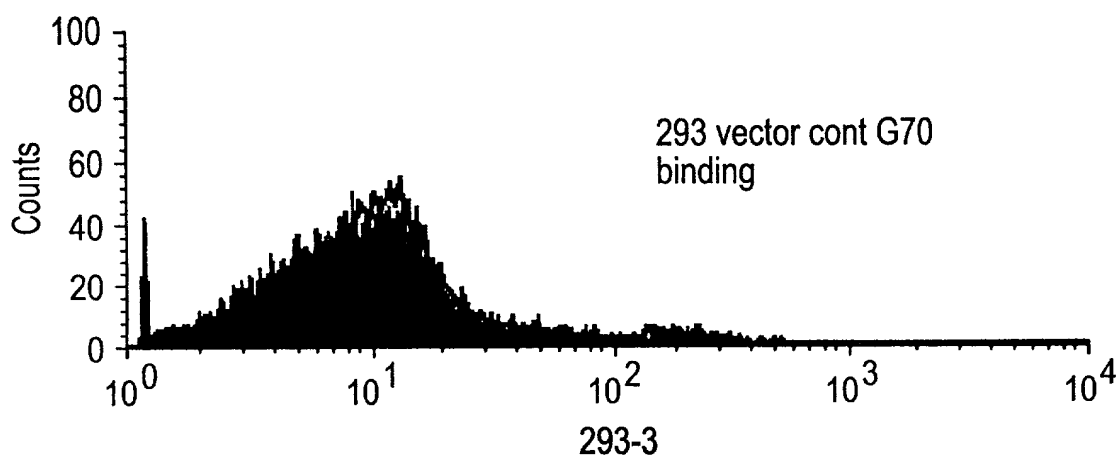


FIG. 16A

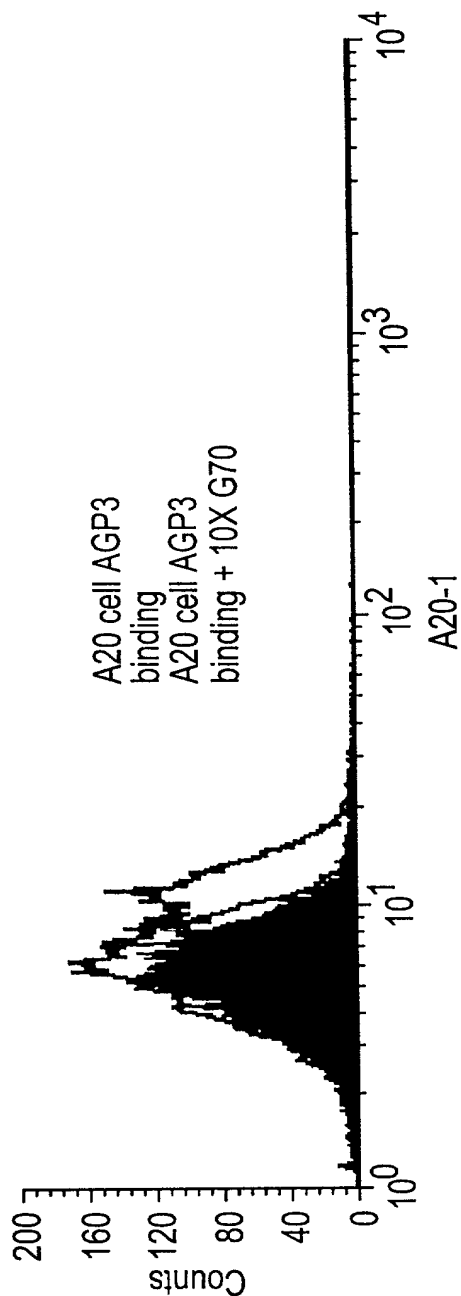
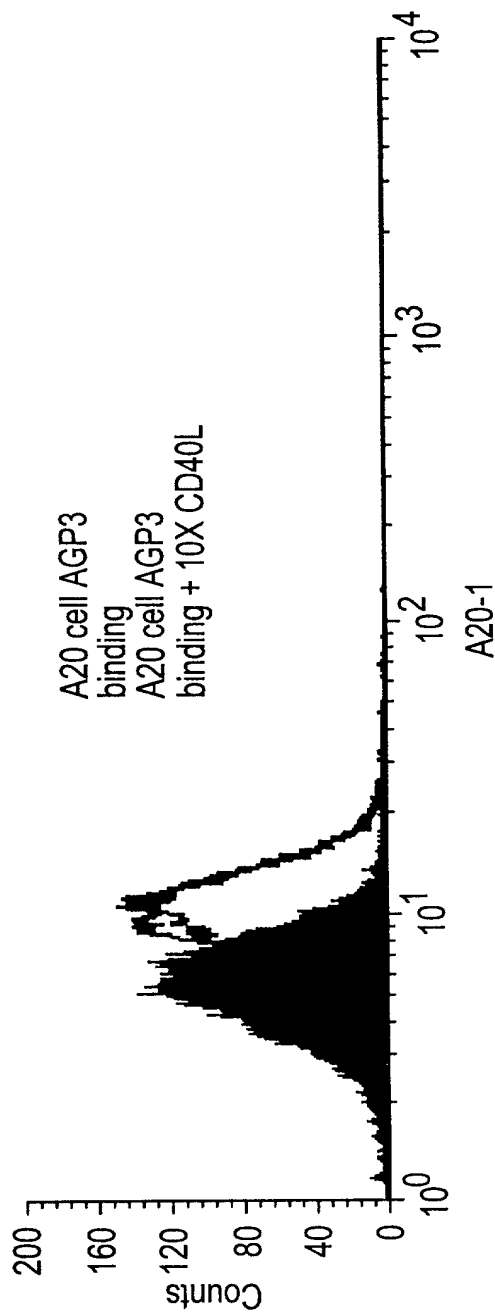


FIG. 16B



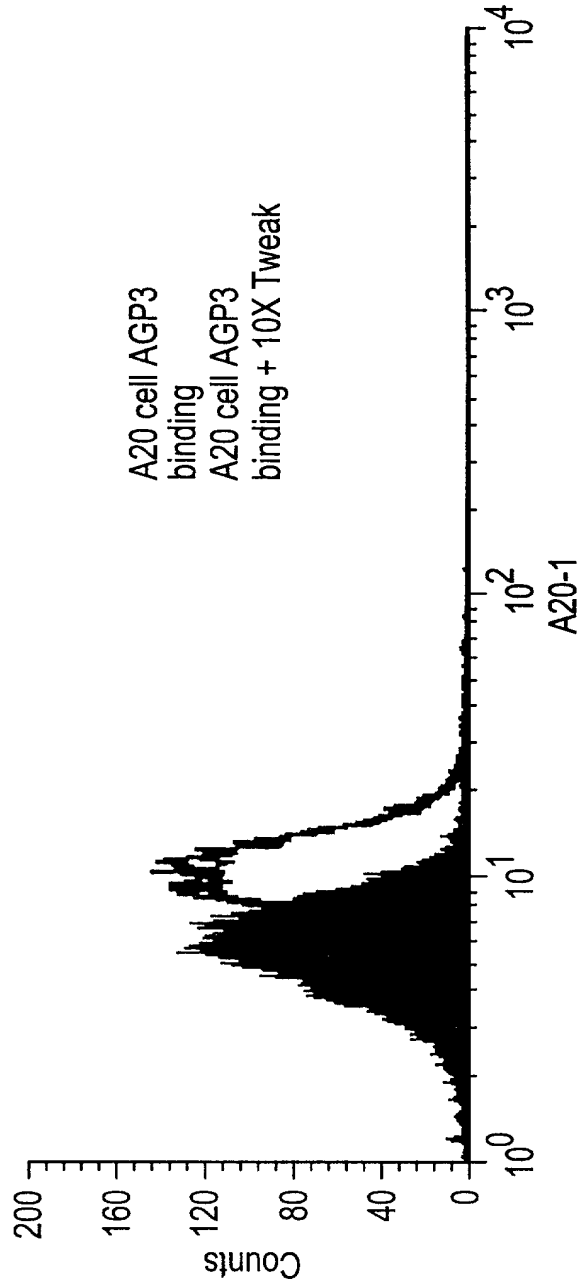


FIG. 16C

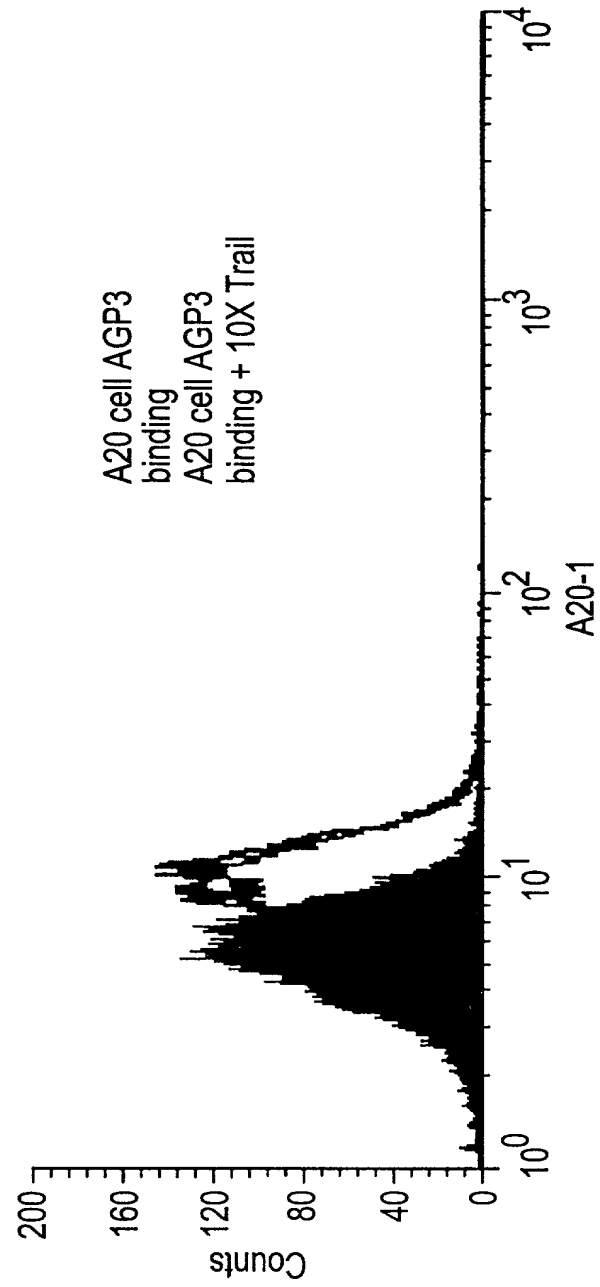


FIG. 16D

FIG. 16C

FIG. 17A

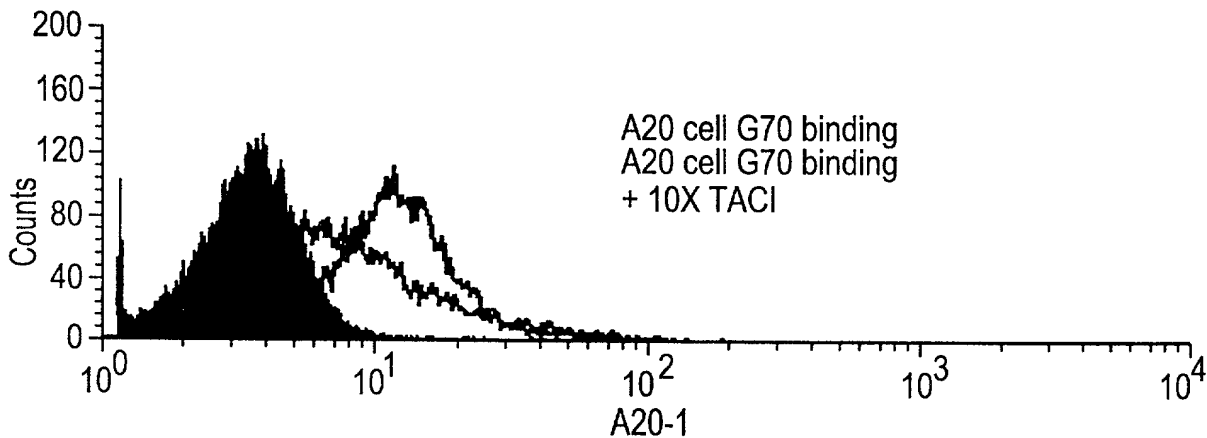


FIG. 17B

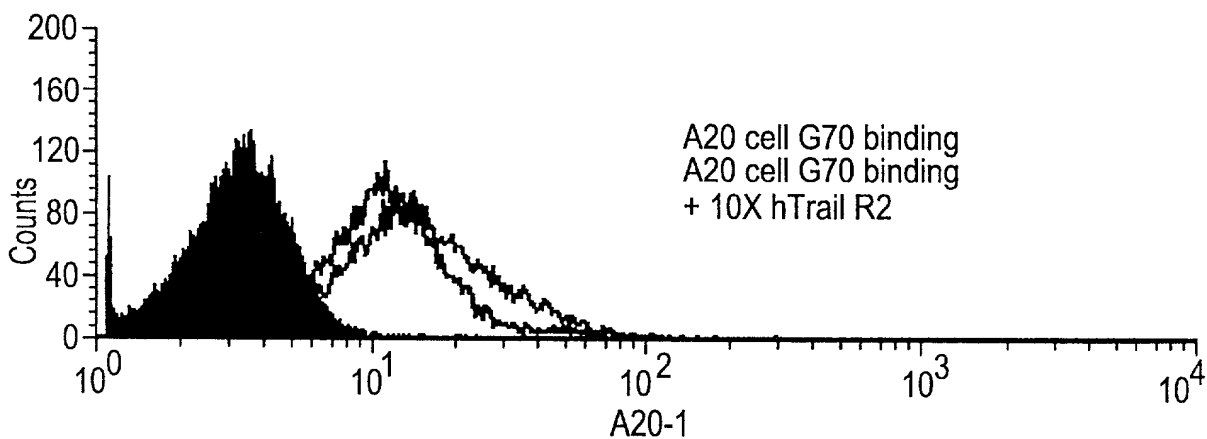


FIG. 17C

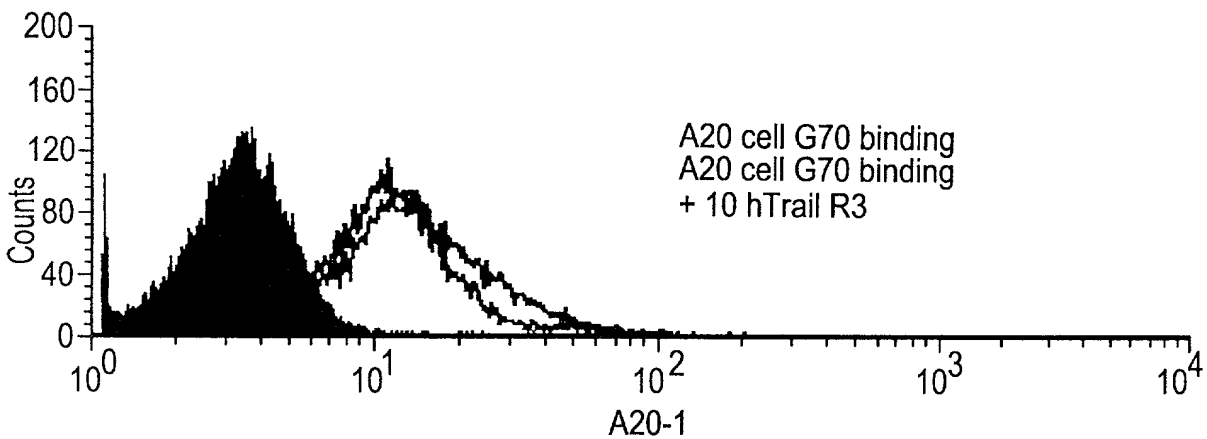


FIG. 18

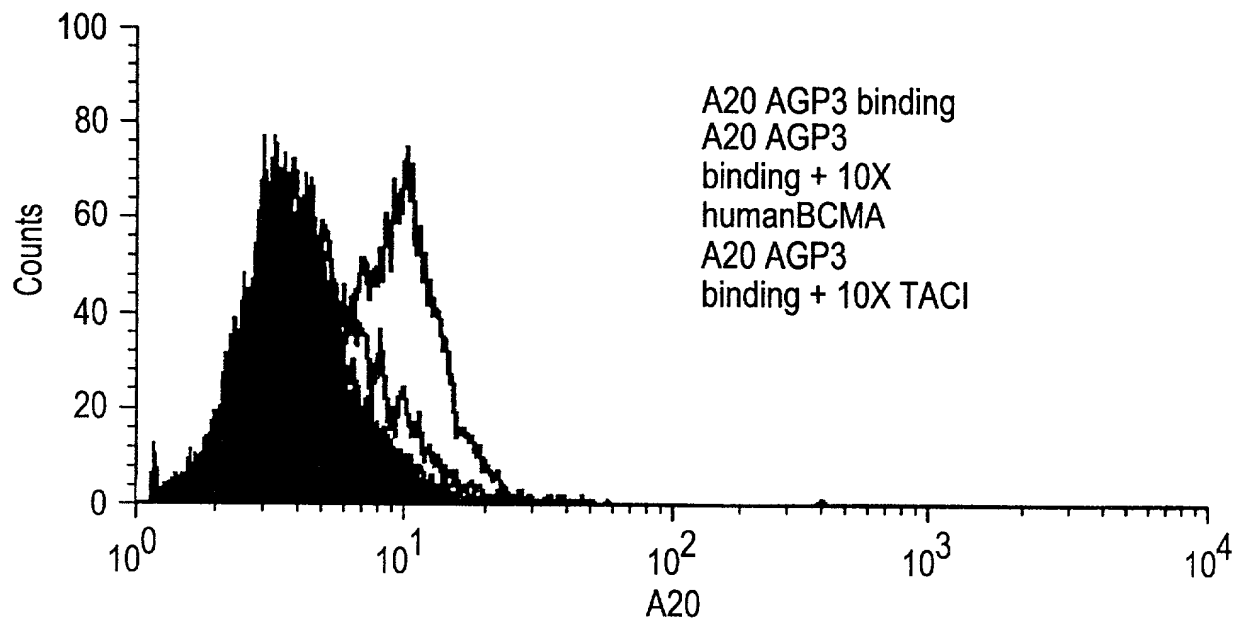


FIG. 19A

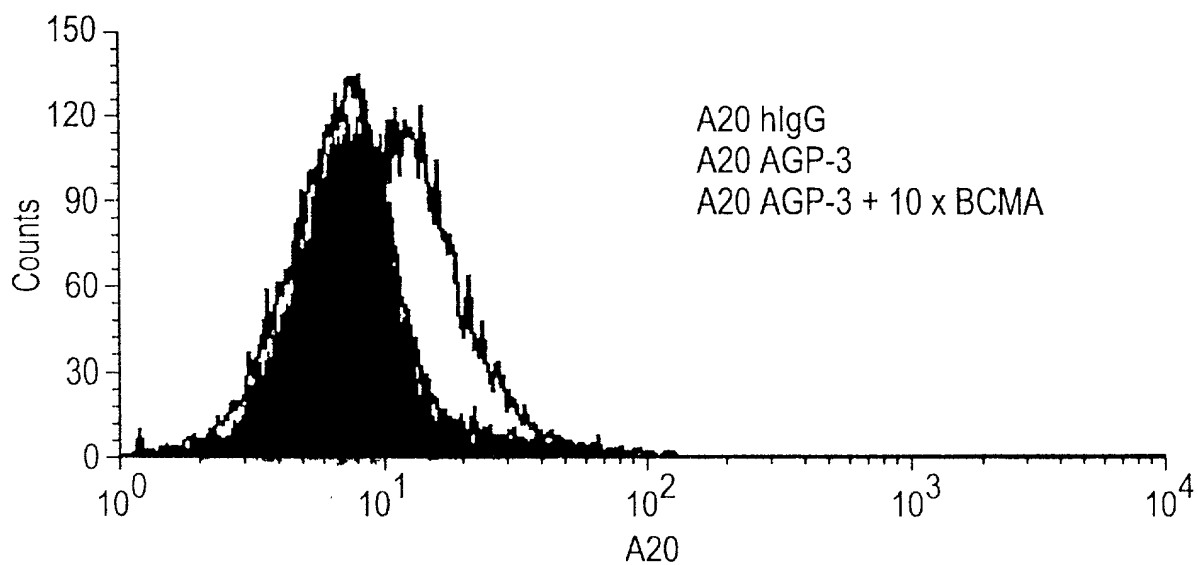


FIG. 19B

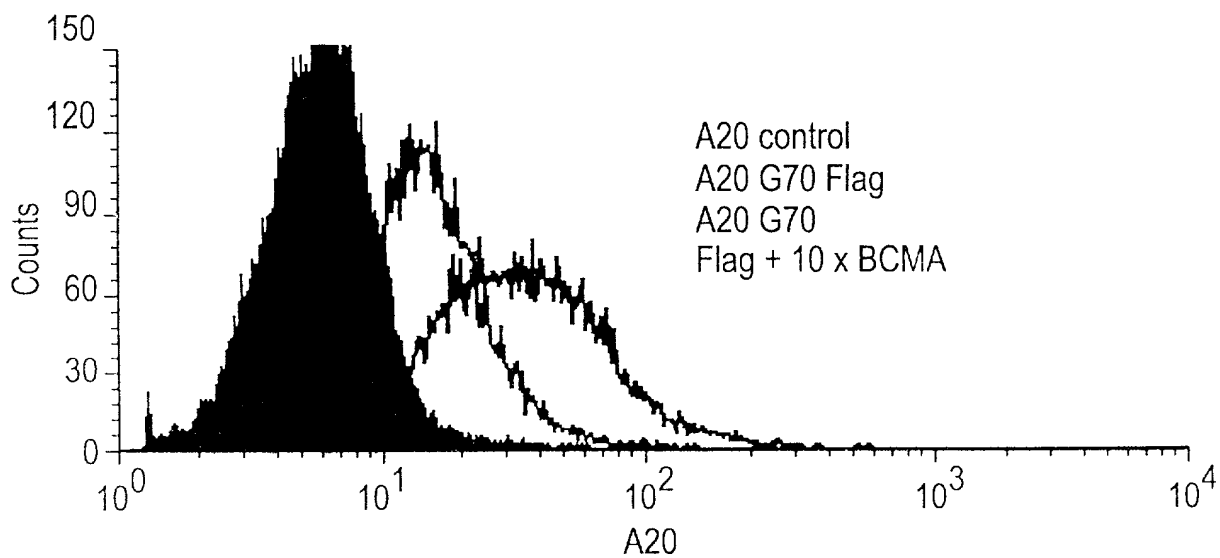


FIG. 20A

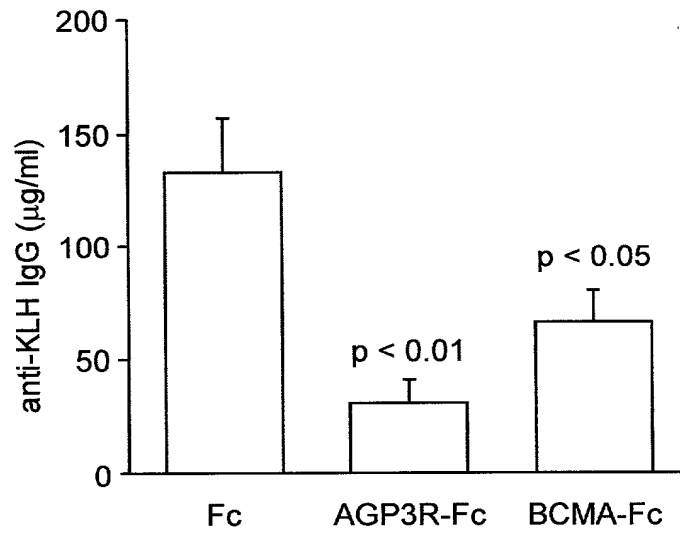


FIG. 20B

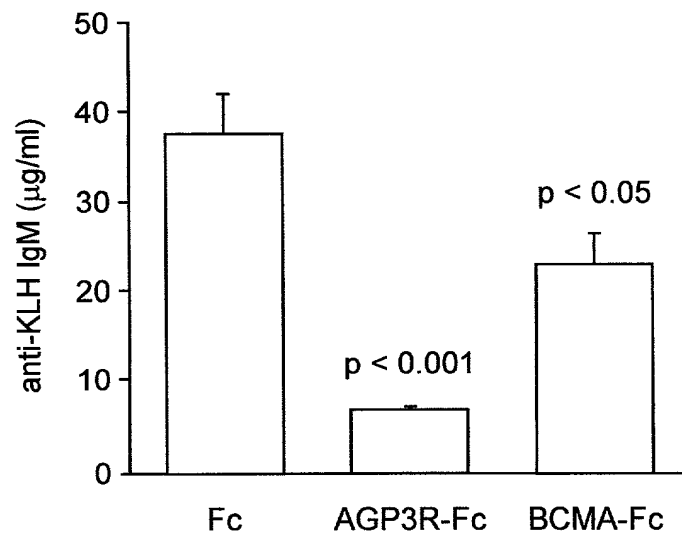


FIG. 20C

